Can AI help to estimate the global burden of AMR?

Catrin Moore, 5th June 2019

Institute for Health Metrics and Evaluation
UNIVERSITY of WASHINGTON
IHME MORU Tropical Health Network GRAM Global Research on Antimicrobial Resistance
BIG DATA INSTITUTE UNIVERSITY OF OXFORD

Outline for talk

1. **What is the Global Research on AntiMicrobial resistance (GRAM) study**
2. The challenges for the study
3. How AI might be able to assist

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The GRAM project Team

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- Susanna Dunachie
- Bahar Kashef Hamdani
- Christine Boinett

Impact of AMR in different regions

Global burden of AMR disease estimates to date

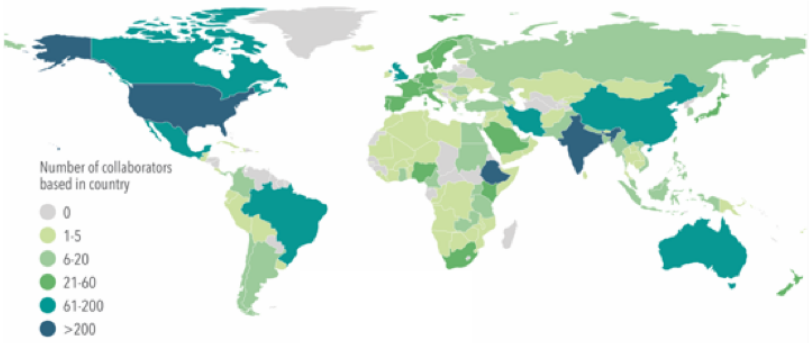
- **25,000 EU deaths pa (2009)** from a selected list of resistant bacteria (excl TB) - ECDC
- **700,000 global deaths pa** from resistant HIV, malaria, TB, *E.coli, K. pneumoniae* and *S. aureus* (O'Neill report 2016)
- **19,122 Thai deaths (2010),** hospital-acquired infection attributed to AMR (Lim et al, Elife 2016)
- **126,000 global deaths (2016)** resistant TB (GBD Lancet 2017)
- **23,000 US deaths pa** https://www.cdc.gov/drugresistance/
- **33,000 EU deaths pa (2015)** due to AMR (EARS-Net/ECDC); 39% of the burden caused by infections with bacteria resistant to last-line antibiotics (eg carbapenems and colistin)

Different methodologies, data sources, and infection focus makes comparison not possible

Key Objectives of the GRAM project

1. Comprehensive and up-to-date global data synthesis of AMR of (selected) bacterial pathogens
2. Geospatial mapping of the distribution of resistance of selected bug-drug combinations
3. Incorporation of the mortality and morbidity caused by these AMR bacterial pathogens into the GBD Study estimates

Global Collaboration for a global study:
3,034 co-investigators in 138 countries and 3 non-sovereign locations



List of bacteria and antibiotics

- **Generate accurate and timely estimates on the magnitude and trends in AMR burden** for 17 "bug-drug" combinations across the world, which can be used to:
  - Inform treatment guidelines
  - Set agendas for decision-making and research
  - Monitor trends globally
  - Facilitate the assessment of interventions over time
  - Detect emerging problems

Bacteria	Antibacterial drug(s)
Escherichia coli	Third-generation cephalosporins, fluoroquinolones
Shigella	Fluoroquinolones
Klebsiella pneumoniae	Third-generation cephalosporins, carbapenems
Streptococcus pneumoniae	Penicillin
Staphylococcus aureus	Methicillin
Salmonella Typhi and Paratyphi	Fluoroquinolones, chloramphenicol
Non-typhoidal *Salmonellae*	Fluoroquinolones
Neisseria gonorrhoeae	Third-generation cephalosporins
Mycobacterium tuberculosis	First-line – isoniazid, rifampicin, second-line – fluoroquinolones, amikacin, capreomycin, kanamycin

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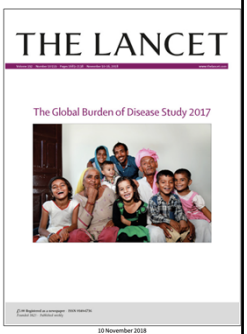

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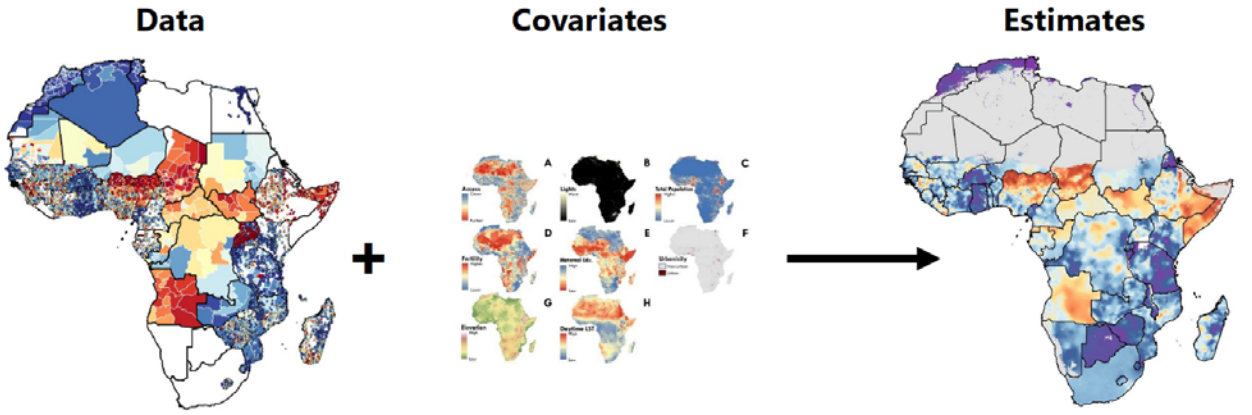
Geostatistical modelling: Methods



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Data: Systematic Reviews

Pathogen	Search Strategy	Starting library	Title/Abstract Screening - Included	Full text found	Full text screening	Papers extracted	Isolates (N)	Database clean	Analysis
Salmonella enterica Typhi/Paratyphi A	x	4,161		1,363	1,363	629	131,088	x	x
NTS	x								
Shigella species	x	3,633	1,702	1,646	1,646	688	181,307	x	
MTB complex	x	29,275	14,554	5,232	193 Africa only	5			
E. coli, S. aureus, K. pneumoniae, S. pneumoniae	x	72,050	25,506 (46,080 screened)	602					
N. gonorrhoeae	x	search in progress							
A. baumannii	x	search in progress							
P. aeruginosa	x	search in progress							

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Machine Learning for Systematic Reviews

- Given the enormous task all *S. aureus, S. pneumoniae, E. coli* and *K. pneumoniae* papers have been entered into a systematic review software
- Inclusion/exclusion:
  - Papers already included and excluded by reviewers informed the inclusion/exclusion criteria, a custom classifier model was built
  - This model provided bins for those left to screen (next slide) to concentrate efforts
- We are working to extract from the written information in the manuscript based on natural language formation (NLF)
- Also working on an R script to extract data from tables

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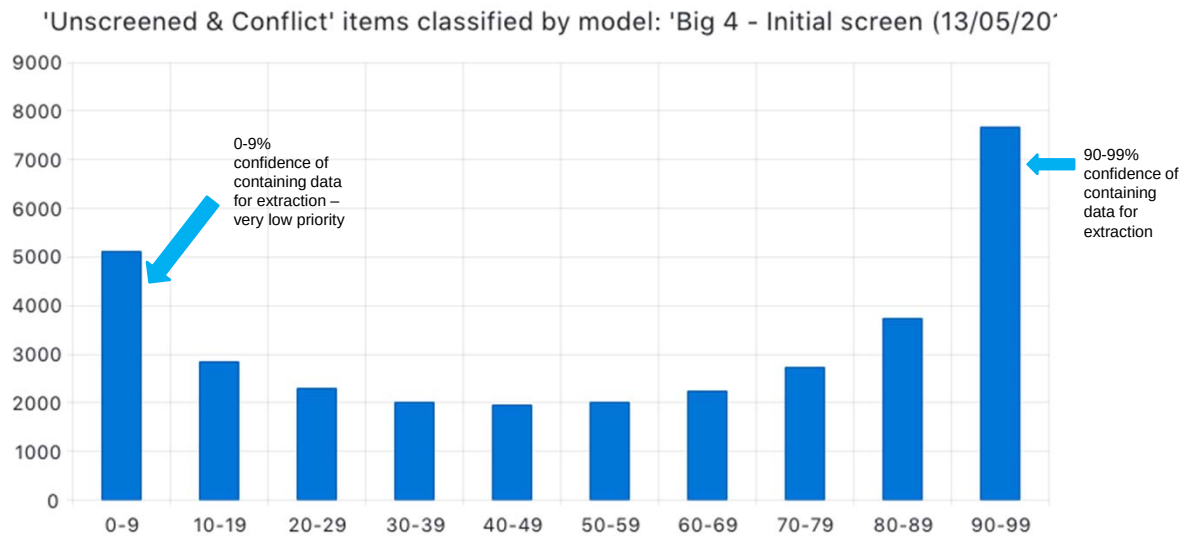

X axis provides confidence of inclusion based upon papers already screened

Thank you!

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